AMENDMENTS TO THE CLAIMS

Please rewrite the claims as follows. A complete listing of the claims is provided below, in accordance with the provisions of 37 CFR 1.121.

1. (Withdrawn) A method of producing an Isotope Map for data from a mass spectrometric injection of a biological sample comprising:

   a) performing Noise reduction and Centroiding with a Noise Reduction Module on said data from a mass spectometric injection of a biological sample, and

   b) generating an Isotope Map from the noise reduced and centroided data, thereby producing an Isotope Map.

2. (Withdrawn) The method of claim 1, wherein said biological sample is comprised of unlabeled biomolecules.

3. (Withdrawn) The method of claim 1, wherein said biological sample is comprised of underivatized biomolecules.

4. (Withdrawn) The method of claim 1, wherein said biological sample is comprised of biomolecules that are both unlabeled and underivatized.

5. (Withdrawn) The method of claim 1, wherein said biological sample is comprised of cleaved biomolecules.

6. (Withdrawn) The method of claim 5, wherein said biomolecules are cleaved with an enzyme.

7. (Withdrawn) The method of claim 6, wherein said enzyme is trypsin.

8. (Withdrawn) A method for producing a Peptide Map from an Isotope Map for data from a mass spectometric injection of a biological sample comprising:

   a) performing Peptide Detection on an Isotope Map with a Peptide Detection Module, and

b) generating a Peptide Map from the results of the peptide detection, thereby producing a Peptide Map.

9. (Cancelled)

10. (Cancelled)

11. (Previously Presented) The method of claim 61, further comprising determining the differential intensities of the matched biomolecules between the aligned peptide maps of step (e), thereby determining differentially expressed biomolecules between the two or more biological samples.

12. (Cancelled)

13. (Withdrawn) A computer implemented method of producing an Isotope Map for data from a mass spectometric injection of a biological sample comprising:

a) inputting data from a mass spectometric injection of a biological sample, and performing Noise reduction and Centroiding with a Noise Reduction Module on said, and

b) generating an Isotope Map from the noise reduced and centroided data, thereby producing an Isotope Map.

14. (Withdrawn) The computer implemented method of claim 13, wherein said biological sample is comprised of unlabeled biomolecules.

15. (Withdrawn) The computer implemented method of claim 13, wherein said biological sample is comprised of underivatized biomolecules.

16. (Withdrawn) The computer implemented method of claim 13, wherein said biological sample is comprised of biomolecules that are both unlabeled and underivatized.

17. (Withdrawn) The computer implemented method of claim 13, wherein said biological sample is comprised of cleaved biomolecules.

18. (Withdrawn) The computer implemented method of claim 17, wherein said biomolecules are cleaved with an enzyme.

19. (Withdrawn) The computer implemented method of claim 18, wherein said enzyme is trypsin.

20. (Withdrawn) A computer implemented method for producing a Peptide Map from an Isotope Map for data from a mass spectometric injection of a biological sample comprising:

a) inputting an Isotope Map;

b) performing Peptide Detection on said Isotope Map with a Peptide Detection Module, and

c) generating a Peptide Map from the results of the peptide detection, thereby producing a Peptide Map.

21. (Cancelled)

22. (Cancelled)

23. (Previously Presented) The computer implemented method of claim 71, further comprising determining the differential intensities of the matched biomolecules between the aligned peptide maps of step (e), thereby determining differentially expressed biomolecules between the two or more biological samples.

24. (Cancelled)

25. (Withdrawn) A computer-readable memory having stored thereon a program for producing an Isotope Map for data from a mass spectometric injection of a biological sample comprising:

a) computer code that receives as input data from a mass spectometric injection of a biological sample, and performing Noise reduction and Centroiding with a Noise Reduction Module on said, and

b) and computer code that generates an Isotope Map from the noise reduced and centroided data, thereby producing an Isotope Map.

26. (Withdrawn) The computer-readable memory of claim 25, wherein said biological sample is comprised of unlabeled biomolecules.

27. (Withdrawn) The computer-readable memory of claim 25, wherein said biological sample is comprised of underivatized biomolecules.

28. (Withdrawn) The computer-readable memory of claim 25, wherein said biological sample is comprised of biomolecules that are both unlabeled and underivatized.

29. (Withdrawn) The computer-readable memory of claim 25, wherein said biological sample is comprised of cleaved biomolecules.

30. (Withdrawn) The computer-readable memory of claim 29, wherein said biomolecules are cleaved with an enzyme.

31. (Withdrawn) The computer-readable memory of claim 30, wherein said-enzyme is trypsin.

32. (Withdrawn) A computer-readable memory having stored thereon a program for producing a Peptide Map from an Isotope Map for data from a mass spectometric injection of a biological sample comprising:

a) computer code that receives as input an Isotope Map;

b) computer code that performs Peptide Detection on said Isotope Map with a Peptide Detection Module, and

c) computer code that generates a Peptide Map from the results of the peptide detection, thereby producing a Peptide Map.

33. (Cancelled)

34. (Cancelled)

35. (Previously Presented) The computer- usable media of claim 101, having computer readable code embodied therein for causing a computer to determine the differential intensities of the matched biomolecules between the aligned peptide maps of step (e), thereby determining differentially expressed biomolecules between the two or more biological samples.

36. (Cancelled)

37. (Withdrawn) A computer system for producing an Isotope Map for data from a mass spectometric injection of a biological sample comprising a processor and a memory coupled to said processor, said memory encoding one or more programs, said one or more programs causing said processor to perform a method comprising:

a) computer code that receives as input data from a mass spectometric injection of a biological sample, and performing Noise reduction and Centroiding with a Noise Reduction Module on said, and

b) computer code that generates an Isotope Map from the noise reduced and centroided data, thereby producing an Isotope Map.

38. (Withdrawn) The computer system of claim 37, wherein said biological sample is comprised of unlabeled biomolecules.

39. (Withdrawn) The computer system of claim 37, wherein said biological sample is comprised of underivatized biomolecules.

40. (Withdrawn) The computer system of claim 37, wherein said biological sample is comprised of biomolecules that are both unlabeled and underivatized.

41. (Withdrawn) The computer system of claim 37, wherein said biological sample is comprised of cleaved biomolecules.

42. (Withdrawn) The computer system of claim 41, wherein said biomolecules are cleaved with an enzyme.

43. (Withdrawn) The computer system of claim 42, wherein said enzyme is trypsin.

44. (Withdrawn) A computer system for producing a Peptide Map from an Isotope Map for data from a mass spectometric injection of a biological sample comprising a processor and a memory coupled to said processor, said memory encoding one or more programs, said one or more programs causing said processor to perform a method comprising:

a) computer code that receives as input an Isotope Map;

b) computer code that performs Peptide Detection on said Isotope Map with a Peptide Detection Module, and

c) computer code that generates a Peptide Map from the results of the peptide detection, thereby producing a Peptide Map.

45. (Cancelled)

46. (Cancelled)

47. (Previously Presented) The computer system of claim 81, wherein said method performed by said processor further comprises determining the differential intensities of the matched biomolecules between the aligned peptide maps of step (e), thereby determining differentially expressed biomolecules between the two or more biological samples.

48. (Cancelled)

49. (Withdrawn) A method for displaying information on an Isotope Map for data from a mass spectometric injection of a biological sample comprising:

a) inputting data from a mass spectometric injection of a biological sample;

b) performing Noise reduction and Centroiding with a Noise Reduction Module on said data;

c) generating an Isotope Map from the noise reduced and centroided data, thereby producing an Isotope Map, and

d) displaying information on said Isotope Map to a user.

50. (Withdrawn) The method of claim 49, wherein said biological sample is comprised of unlabeled biomolecules.

51. (Withdrawn) The method of claim 49, wherein said biological sample is comprised of underivatized biomolecules.

52. (Withdrawn) The method of claim 49, wherein said biological sample is comprised of biomolecules that are both unlabeled and underivatized.

53. (Withdrawn) The method of claim 49, wherein said biological sample is comprised of cleaved biomolecules.

54. (Withdrawn) The method of claim 53, wherein said biomolecules are cleaved with an enzyme.

55. (Withdrawn) The method of claim 54, wherein said enzyme is trypsin.

56. (Withdrawn) A method for displaying information on a Peptide Map produced from an Isotope Map for data from a mass spectometric injection of a biological sample comprising:

a) inputting an Isotope Map;

b) performing Peptide Detection on said Isotope Map with a Peptide Detection Module;

c) generating a Peptide Map from the results of the peptide detection, thereby producing a Peptide Map, and

d) displaying information on said Peptide Map to a user.

57. (Cancelled)

58. (Cancelled)

59. (Previously Presented) The method of claim 91, further comprising determining the differential intensities of the matched biomolecules between the aligned peptide maps of step (e), thereby determining differentially expressed biomolecules between the two or more biological samples, and displaying information on said differential intensities to the user.

60. (Cancelled)

61. (Currently Amended) A method for matching a plurality of biomolecules between two or more biological samples comprising:

a) obtaining mass-to-charge ratio data, chromatographic retention time data and ion intensity data corresponding to biomolecules of two or more biological

samples that have been separated and detected by liquid chromatography coupled with mass spectrometry;

b) ~~obtaining~~ generating peptide maps from the data corresponding to the biological samples, the peptide maps comprising mass-to-charge ratio (m/z) co-ordinates, ion intensity coordinates, and chromatography retention time co-ordinates;

c) deriving a retention time transformation function that corrects for differences in ~~chromatography~~ chromatographic retention time between the peptide maps;

d) applying the derived retention time transformation function to ~~one of~~ the peptide maps to align the peptide maps thereby matching a plurality of biomolecules between two or more biological samples ~~obtain a transformed retention time for each of the detected biomolecules, thereby aligning the peptide maps of each biological sample~~; and

e) ~~identifying as matching biomolecules corresponding to aligned peptide maps that are within a m/z and transformed retention time tolerance~~ outputting the aligned peptide maps to a user.

62. (Previously Presented) The method of claim 61, wherein the liquid chromatography coupled with mass spectrometry comprises liquid chromatography-mass spectrometry (LC-MS) or liquid chromatography-mass spectrometry/mass spectrometry (LC-MS/MS).

63. (Withdrawn) The method of claim 62, wherein in step (a) at least one of the biological samples has been separated and detected by liquid chromatography coupled with mass spectrometry (LC-MS) and at least one of the biological samples has been separated and detected by liquid chromatography-mass spectrometry/mass spectrometry (LC-MS/MS).

64. (Previously Presented) The method of claim 62, wherein in step (a) all of the biological samples have been separated and detected by liquid chromatography coupled with mass spectrometry (LC-MS).

65. (Withdrawn) The method of claim 62, wherein in step (a) all of the biological samples have been separated and detected by liquid chromatography-mass spectrometry/mass spectrometry (LC-MS/MS).

66. (Previously Presented) The method of claim 61, wherein the data of step (a) is obtained by performing liquid chromatography coupled with mass spectrometry immediately before performing step (b).

67. (Withdrawn) The method of claim 61, wherein the data of step (a) is obtained by retrieving the data from data files stored in memory associated with a computer system.

68. (Previously Presented) The method of claim 61, wherein the peptide map of step (b) is obtained by performing peptide detection on the data obtained in step (a) immediately before performing step (c).

69. (Withdrawn) The method of claim 61, wherein the peptide map of step (b) is obtained by retrieving the peptide map from data files stored in memory associated with a computer system.

70. (Previously Presented) The method of claim 61, further comprising determining the differential intensities of the unmatched biomolecules between the aligned peptide maps of step (e), thereby determining uniquely expressed biomolecules between the two or more biological samples.

71. (Currently Amended) A computer-implemented method for matching a plurality of biomolecules between two or more biological samples comprising:

a) obtaining mass-to-charge ratio data, chromatographic retention time data and ion intensity data corresponding to biomolecules of two or more biological samples that have been separated and detected by liquid chromatography coupled with mass spectrometry;

b) ~~obtaining~~ generating peptide maps from the data corresponding to the biological samples, the peptide maps comprising mass-to-charge ratio (m/z) co-ordinates, ion intensity coordinates, and chromatography retention time co-ordinates;

c) deriving a retention time transformation function that corrects for differences in ~~chromatography~~ chromatographic retention time between the peptide maps;

d) applying the derived retention time transformation function to ~~one of~~ the peptide maps to align the peptide maps thereby matching a plurality of biomolecules between two or more biological samples ~~obtain a transformed retention time for each of the detected biomolecules, thereby aligning the peptide maps~~; and

e) ~~identifying as matching biomolecules corresponding to aligned peptide maps that are within a m/z and transformed retention time tolerance~~ storing data identifying the matched biomolecules in a computer memory.

72. (Previously Presented) The method of claim 71, wherein the liquid chromatography coupled with mass spectrometry comprises liquid chromatography-mass spectrometry (LC-MS) or liquid chromatography-mass spectrometry/mass spectrometry (LC-MS/MS).

73. (Withdrawn) The method of claim 72, wherein at least one of the biological samples has been separated and detected by liquid chromatography coupled with mass spectrometry (LC-MS) and at least one of the biological samples has been separated and detected by liquid chromatography-mass spectrometry/mass spectrometry (LC-MS/MS).

74. (Previously Presented) The method of claim 72, wherein in step (a) all of the biological samples have been separated and detected by liquid chromatography coupled with mass spectrometry (LC-MS).

75. (Withdrawn) The method of claim 72, wherein in step (a) all of the biological samples have been separated and detected by liquid chromatography-mass spectrometry/mass spectrometry (LC-MS/MS).

76. (Previously Presented) The method of claim 71, wherein the data of step (a) is obtained by performing liquid chromatography coupled with mass spectrometry immediately before performing step (b).

77. (Withdrawn) The method of claim 71, wherein the data of step (a) is obtained by retrieving the data from data files stored in memory associated with a computer system.

78. (Previously Presented) The method of claim 71, wherein the peptide map is obtained by performing peptide detection on the data obtained in step (a) immediately before performing step (c).

79. (Withdrawn) The method of claim 71, wherein the peptide map is obtained by retrieving the peptide map from data files stored in memory associated with a computer system.

80. (Previously Presented) The method of claim 71, further comprising determining the differential intensities of the unmatched biomolecules between the aligned peptide maps of step (e), thereby determining uniquely expressed biomolecules between the two or more biological samples.

81. (Currently Amended) A system for matching biomolecules between two or more biological samples, the system comprising at least one processor, memory coupled to the processor, and computer programming configured to cause the processor to:

a) receive as input mass-to-charge ratio data, chromatographic retention time data and ion intensity data corresponding to biomolecules of two or more biological samples that have been separated and detected by liquid chromatography coupled with mass spectrometry;

b) receive as input peptide maps from the data corresponding to the biological samples, the peptide maps comprising mass-to-charge ratio (m/z) co-ordinates, ion intensity coordinates, and chromatography retention time co-ordinates corresponding to said biomolecules;

c) derive a retention time transformation function that corrects for differences in ~~chromatography~~ chromatographic retention time between the peptide maps;

d) apply the derived retention time transformation function to ~~at least one of~~ the peptide maps to align the peptide maps thereby matching a plurality of biomolecules between two or more biological samples. ~~obtain a transformed retention time for each of the detected biomolecules, thereby aligning the peptide maps of each biological sample;~~ and

~~e) identify as matching biomolecules corresponding to aligned peptide maps that are within a m/z and transformed retention time tolerance~~ store data identifying the matched biomolecules in a computer memory.

82. (Previously Presented) The computer system of claim 81, wherein the liquid chromatography coupled with mass spectrometry comprises liquid chromatography-mass spectrometry (LC-MS) or liquid chromatography-mass spectrometry/mass spectrometry (LC-MS/MS).

83. (Withdrawn) The computer system of claim 82, wherein at least one of the biological samples has been separated and detected by liquid chromatography coupled with mass spectrometry (LC-MS) and at least one of the biological samples has been separated and detected by liquid chromatography-mass spectrometry/mass spectrometry (LC-MS/MS).

84. (Previously Presented) The computer system of claim 82, wherein in step (a) all of the biological samples have been separated and detected by liquid chromatography coupled with mass spectrometry (LC-MS).

85. (Withdrawn) The computer system of claim 82, wherein in step (a) all of the biological samples have been separated and detected by liquid chromatography-mass spectrometry/mass spectrometry (LC-MS/MS).

86. (Previously Presented) The computer system of claim 81, wherein the data of step (a) is obtained by performing liquid chromatography coupled with mass spectrometry immediately before performing step (b).

87. (Withdrawn) The computer system of claim 81, wherein the data of step (a) is obtained by retrieving the data from data files stored in memory associated with a computer system.

88. (Previously Presented) The computer system of claim 81, wherein the peptide map of step (b) is obtained by performing peptide detection on the data obtained in step (a) immediately before performing step (c).

89. (Withdrawn) The computer system of claim 81, wherein the peptide map of step (b) is obtained by retrieving the peptide map from data files stored in memory associated with a computer system.

90. (Previously Presented) The computer system of claim 81, wherein said method performed by said processor further comprises determining the differential intensities of the unmatched biomolecules between the aligned peptide maps of step (e), thereby determining uniquely expressed biomolecules between the two or more biological samples.

91. (Currently Amended) A method for displaying information on matching a plurality of biomolecules between two or more biological samples comprising:

a) inputting mass-to-charge ratio data, chromatographic retention time data and ion intensity data corresponding to biomolecules in two or more biological samples that have been separated and detected by liquid chromatography coupled with mass spectrometry;

b) inputting peptide maps from the data corresponding to the biological samples, the peptide maps comprising mass-to-charge ratio (m/z) co-ordinates, ion intensity coordinates, and chromatography retention time co-ordinates for each biomolecule in each biological sample;

c) deriving a retention time transformation function that corrects for differences in ~~chromatography~~ chromatographic retention time between the peptide maps;

d) applying the derived retention time transformation function to one of the peptide maps to align the peptide maps thereby matching a plurality of biomolecules between two or more biological samples; and ~~obtain a transformed retention time for the detected biomolecules, thereby aligning the peptide maps of each biological sample;~~

e) ~~identifying as matching biomolecules corresponding to aligned peptide maps that are within a m/z and transformed retention time tolerance; and~~

~~f)~~ displaying information on said matching to a user.

92. (Previously Presented) The method of claim 91, wherein the liquid chromatography coupled with mass spectrometry comprises liquid chromatography-mass spectrometry (LC-MS) or liquid chromatography-mass spectrometry/mass spectrometry (LC-MS/MS).

93. (Withdrawn) The method of claim 92, wherein at least one of the biological samples has been separated and detected by liquid chromatography coupled with mass spectrometry (LC-MS) and at least one of the biological samples has been separated and detected by liquid chromatography-mass spectrometry/mass spectrometry (LC-MS/MS).

94. (Previously Presented) The method of claim 92, wherein in step (a) all of the biological samples have been separated and detected by liquid chromatography coupled with mass spectrometry (LC-MS).

95. (Withdrawn) The method of claim 92, wherein in step (a) all of the biological samples have been separated and detected by liquid chromatography-mass spectrometry/mass spectrometry (LC-MS/MS).

96. (Previously Presented) The method of claim 91, wherein the data of step (a) is obtained by performing liquid chromatography coupled with mass spectrometry immediately before performing step (b).

97. (Withdrawn) The method of claim 91, wherein the data of step (a) is obtained by retrieving the data from data files stored in memory associated with a computer system.

98. (Previously Presented) The method of claim 91, wherein the peptide map of step (b) is obtained by performing peptide detection on the data obtained in step (a) immediately before performing step (c).

99. (Withdrawn) The method of claim 91, wherein the peptide map of step (b) is obtained by retrieving the peptide map from data files stored in memory associated with a computer system.

100. (Previously Presented) The method of claim 91, further comprising determining the differential intensities of the unmatched biomolecules between the aligned peptide maps of step (e), thereby determining uniquely expressed biomolecules between the two or more biological samples.

101. (Currently Amended) Stored ~~C~~computer usable media having computer readable code embodied therein for causing a computer to:

a) receive as input mass-to-charge ratio data, chromatographic retention time data and ion intensity data corresponding to biomolecules of two or more biological samples that have been separated and detected by liquid chromatography coupled with mass spectrometry;

b) receive as input peptide maps from the data corresponding to the biological samples, the peptide maps containing mass-to-charge ratio (m/z) co-ordinates, ion intensity coordinates, and chromatography retention time co-ordinates;

c) derive a retention time transformation function that corrects for differences in chromatography retention time between the peptide maps; and

d) apply the derived retention time transformation function to one of the peptide maps to align the peptide maps thereby matching a plurality of biomolecules between two or more biological samples. ~~obtain a transformed retention time for each of the detected biomolecules, thereby aligning the peptide maps of each biological sample;~~ and

~~e) identify as matching biomolecules corresponding to the aligned peptide maps that are within a m/z and transformed retention time tolerance.~~ storing data identifying the matched biomolecules in a computer memory.

102. (Currently Amended) The stored ~~computer-readable memory~~ computer usable media of claim 101, wherein the liquid chromatography coupled with mass

spectrometry comprises liquid chromatography-mass spectrometry (LC-MS) or liquid chromatography-mass spectrometry/mass spectrometry (LC-MS/MS).

103. (Withdrawn) The computer usable memory of claim 102, wherein at least one of the biological samples has been separated and detected by liquid chromatography coupled with mass spectrometry (LC-MS) and at least one of the biological samples has been separated and detected by liquid chromatography-mass spectrometry/mass spectrometry (LC-MS/MS).

104. (Currently Amended) The stored ~~computer-readable memory~~ computer usable media of claim 102, wherein in part (a) all of the biological samples have been separated and detected by liquid chromatography coupled with mass spectrometry (LC-MS).

105. (Withdrawn) The computer usable memory of claim 102, wherein in part (a) all of the biological samples have been separated and detected by liquid chromatography-mass spectrometry/mass spectrometry (LC-MS/MS).

106. (Currently Amended) The stored ~~computer-readable memory~~ computer usable media of claim 101, wherein the data of part (a) is obtained by performing liquid chromatography coupled with mass spectrometry immediately before performing part (b).

107. (Withdrawn) The computer usable memory of claim 101, wherein the data of part (a) is obtained by retrieving the data from data files stored in memory accessible by the processor.

108. (Currently Amended) The stored ~~computer-readable memory~~ computer usable media of claim 101, wherein the peptide map of part (b) is obtained by performing peptide detection on the data obtained in part (a) immediately before performing part (c).

109. (Withdrawn) The computer-usable memory of claim 101, wherein the peptide map of part (b) is obtained by retrieving the peptide map from data files stored in memory accessible by the processor.

110. (Currently Amended) The stored ~~computer-readable memory~~ computer usable media of claim 101, wherein the program further comprises computer code that determines the differential intensities of the unmatched biomolecules between the aligned peptide maps of part (e), thereby determining uniquely expressed biomolecules between the two or more biological samples.